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Bioinformatical analysis of transcriptional patterns in the *Herpesviridae* family

Peter Oláh, Dóra Tombácz, Nándor Póka and Zsolt Boldogkői
University of Szeged, Hungary

The Transcription Interference Network theory describes a model in which the transcriptional machinery acts as a layer of regulation in its own right. In order to identify common transcriptional patterns and aid in experimental design, we have analyzed strand-specific RNA-sequencing data of three members of the *Herpesviridae* family with respect to bidirectional promoter activity, divergent transcription and antisense RNAs. Further comparisons to publicly available double-stranded DNA virus sequencing data served to establish the effects of coverage and possible PCR artifacts, as well as biases caused by the tightly packed viral genomes and high GC-content. High variability of viral genomes within one strain also has to be taken into consideration, while maintaining the precision of read mapping and splice site detection. Although the dense nature of viral genomes is an advantage in transcriptional interference studies, it makes transcript abundances and isoform expression difficult to quantitate, and requires alternative approaches and the optimization of bioinformatical pipelines.Our findings indicate that the patterns of viral transcription might play an important role in the regulation of gene expression, and can also help in motif-based isolation of viral sequences in metagenomic or infected samples.

Biography

Peter Oláh is a Ph.D. student at the Medical University of Szeged, Hungary, working in the group of prof. Zsolt Boldogkői. The main research area of the group is the characterization of the pseudorabies virus gene expression and its use as a model organism in brain research.